

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/380,276 A

CRF Processing Date: 4/10/2002
 Edited by:
 Verified by: (STIC staff)

ENTERED

#15

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;
☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

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APR 12 2002

TECH CENTER 1600/2900

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

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1646

RAW SEQUENCE LISTING

DATE: 04/11/2002

PATENT APPLICATION: US/09/380,276A

TIME: 10:26:39

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\04112002\I380276A.raw

P-6

2 <110> APPLICANT: Ono Pharmaceutical Co., Ltd.
4 <120> TITLE OF INVENTION: Novel Polypeptides, DNAs encoding the polypeptides, and
utility of the
5 Polypeptides
7 <130> FILE REFERENCE: Q55589
9 <140> CURRENT APPLICATION NUMBER: 09/380,276A
10 <141> CURRENT FILING DATE: 1999-08-27
12 <150> PRIOR APPLICATION NUMBER: JP 9-43143
13 <151> PRIOR FILING DATE: 1997-02-27
15 <150> PRIOR APPLICATION NUMBER: PCT/JP98/00799
16 <151> PRIOR FILING DATE: 1997-02-27
18 <160> NUMBER OF SEQ ID NOS: 10
20 <170> SOFTWARE: PatentIn version 3.0
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22 <211> LENGTH: 1251
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo Sapiens
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31 gatcggtctg gaaactgtgt tccctgcaac cagtgtgggc caggcatgga gttgtctaag 180
33 gaatgtggct tgggctatgg ggaggatgca cagtgtgtga cgtgccggct gcacagggttc 240
35 aaggaggact ggggcttcca gaaatgcaag ccctgtctgg actgcgcagt ggtgaaccgc 300
37 ttccagaagg caaattgttc agccaccagt gatgccatct gcggggactg cttgccagga 360
39 ttttatagga agacgaaact tgtcggtctt caagacatgg agtgtgtgcc ttgtggagac 420
41 cctcctcctc cttacgaacc gcactgtgcc agcaaggcca acctcgtgaa gatcgcgctc 480
43 acggcctcca gcccaaggga cagggcgctg gctgccgcta tctgcagcgc tctggccacc 540
45 gtccctgctg ccctgtctcat cctctgtgtc atctattgta agagacagtt tatggagaag 600
47 aaaccagct ggtctctgcg gtcacaggac attcagtaca acggctctga gctgtcgtgt 660
49 cttgacagac ctcagctcca cgaatatgcc cacagagcct gctgccagtg ccgccgtgac 720
51 tcagtgcaga cctgcggggc ggtgcgcttg ctcccatcca tgtgctgtga ggaggcctgc 780
53 agccccaacc cggcgactct tgggtgtggg gtgcattctg cagccagtct tcaggcaaga 840
55 aacgcaggcc cagccgggga gatggtgcg actttcttcg gatccctcac gcagtccatc 900
57 tgtggcgagt ttccagatgc ctggcctctg atgcagaatc ccatgggtgg tgacaacatc 960
59 tctttttgtg actcttatcc tgaactcaat ggagaagaca ttcattctct caatccagaa 1020
61 cttgaaagct caacgtcttt ggattcaaat agcagtcaag atttggttgg tggggctgtt 1080
63 ccagtccagt ctcattctga aaactttaca gcagctactg atttatctag atataacaac 1140
65 aactggttag aatcagcatc aactcaggat gcactaacta tgagaagcca gctagatcag 1200
67 gagagtggcg ctatcatcca cccagccact cagacgtccc tccaggaagc t 1251
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70 <211> LENGTH: 1704
71 <212> TYPE: DNA
72 <213> ORGANISM: Homo sapiens
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Input Set : A:\PTO.AMC.txt

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77 tactagaaca agagaaaacg tttttcactc ttttagtatt actaggctat ttgtcatgta      120
79 aagtgacttg tgaaacagga gactgtagac agcaagaatt cagggatcgg tctggaaact      180
81 gtgttccctg caaccagtgt gggccaggga tggagttgtc taaggaatgt ggcttcggct      240
83 atggggagga tgcacagtgt gtgacgtgcc ggctgcacag gttcaaggag gactggggct      300
85 tccagaaatg caagccctgt ctggactgcg cagtggtgaa ccgctttcag aaggcaaatt      360
87 gttcagccac cagtgatgcc atctgcgggg actgcttgcc aggattttat aggaagacga      420
89 aacttgctcg ctttcaagac atggagtgtg tgccttggtg agaccctcct cctccttacg      480
91 aaccgcaactg tgccagcaag gtcaacctcg tgaagatcgc gtccaaggcc tccagcccac      540
93 gggacacggc gctggctgcc gttatctgca gcgctctggc caccgtcctg ctggccctgc      600
95 tcatcctctg tgtcatctat tgtaagagac agtttatgga gaagaaaccc agctggctctc      660
97 tgcggtcaca ggacattcag tacaacggct ctgagctgtc gtgtcttgac agacctcagc      720
99 tccacgaata tgcccacaga gcctgctgcc agtgccgcg tgactcagtg cagacctgcg      780
101 ggccggtgcg cttgctccca tccatgtgct gtgaggaggc ctgcagcccc aaccggcgca      840
103 ctcttggttg tggggtgcat tctgcagcca gtcttcaggc aagaaacgca ggcccagccg      900
105 gggagatggt gccgactttc ttccgatccc tcacgcagtc catctgtggc gagttttcag      960
107 atgcctggcc tctgatgcag aatcccatgg gtggtgacaa catctctttt tgtgactctt     1020
109 atcctgaact cactggagaa gacattcatt ctctcaatcc agaacttgaa agctcaacgt     1080
111 ctttggtattc aaatagcagt caagatttgg ttggtggggc tgttccagtc cagtctcatt     1140
113 ctgaaaactt tacagcagct actgatttat ctagatataa caacacactg gtagaatcag     1200
115 catcaactca ggatgcacta actatgagaa gccagctaga tcaggagagt ggcgctatca     1260
117 tccaccagc cactcagacg tccctccagg aagcttaaag aacctgcttc tttctgcagt     1320
119 agaagcgtgt gctggaacct aaagagtact cctttgtag gcttatggac tgagcagtct     1380
121 ggaccttgca tggcttctgg ggcaaaaata aatctgaacc aaactgacgg catttgaagc     1440
123 ctttcagcca gttgcttctg agccagacca gctgtaagct gaaacctcaa tgaataacaa     1500
125 gaaaagactc caggccgact catgatactc tgcacttttc ctacatgaga agcttctctg     1560
127 ccacaaaagt gacttcaaag acggatgggt tgagctggca gcctatgaga ttgtggacat     1620
129 ataacaagaa acagaaatgc cctcatgctt attttcatgg tgattgtggt tttacaagac     1680
131 tgaagacca gagtatactt tttc                                     1704
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135 <211> LENGTH: 1704
136 <212> TYPE: DNA
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140 <221> NAME/KEY: misc_feature
141 <223> OTHER INFORMATION: Origin: human bone marrow stromal cell line HAS303
144 <220> FEATURE:
145 <221> NAME/KEY: CDS
146 <222> LOCATION: (45)..(1295)
148 <220> FEATURE:
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153 <221> NAME/KEY: mat_peptide
154 <222> LOCATION: (120)..(1295)
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158                                     Met Ala Leu Lys
159                                     -25

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161	gtg	cta	cta	gaa	caa	gag	aaa	acg	ttt	ttc	act	ctt	tta	gta	tta	cta	104
162	Val	Leu	Leu	Glu	Gln	Glu	Lys	Thr	Phe	Phe	Thr	Leu	Val	Leu	Leu		
163		-20					-15				-10						
165	ggc	tat	ttg	tca	tgt	aaa	gtg	act	tgt	gaa	aca	gga	gac	tgt	aga	cag	152
166	Gly	Tyr	Leu	Ser	Cys	Lys	Val	Thr	Cys	Glu	Thr	Gly	Asp	Cys	Arg	Gln	
167	-5				-1	1				5					10		
169	caa	gaa	ttc	agg	gat	cgg	tct	gga	aac	tgt	gtt	ccc	tgc	aac	cag	tgt	200
170	Gln	Glu	Phe	Arg	Asp	Arg	Ser	Gly	Asn	Cys	Val	Pro	Cys	Asn	Gln	Cys	
171				15					20					25			
173	ggg	cca	ggc	atg	gag	ttg	tct	aag	gaa	tgt	ggc	ttc	ggc	tat	ggg	gag	248
174	Gly	Pro	Gly	Met	Glu	Leu	Ser	Lys	Glu	Cys	Gly	Phe	Gly	Tyr	Gly	Glu	
175			30					35					40				
177	gat	gca	cag	tgt	gtg	acg	tgc	cgg	ctg	cac	agg	ttc	aag	gag	gac	tgg	296
178	Asp	Ala	Gln	Cys	Val	Thr	Cys	Arg	Leu	His	Arg	Phe	Lys	Glu	Asp	Trp	
179		45					50					55					
181	ggc	ttc	cag	aaa	tgc	aag	ccc	tgt	ctg	gac	tgc	gca	gtg	gtg	aac	cgc	344
182	Gly	Phe	Gln	Lys	Cys	Lys	Pro	Cys	Leu	Asp	Cys	Ala	Val	Val	Asn	Arg	
183	60					65				70					75		
185	ttt	cag	aag	gca	aat	tgt	tca	gcc	acc	agt	gat	gcc	atc	tgc	ggg	gac	392
186	Phe	Gln	Lys	Ala	Asn	Cys	Ser	Ala	Thr	Ser	Asp	Ala	Ile	Cys	Gly	Asp	
187					80					85					90		
189	tgc	ttg	cca	gga	ttt	tat	agg	aag	acg	aaa	ctt	gtc	ggc	ttt	caa	gac	440
190	Cys	Leu	Pro	Gly	Phe	Tyr	Arg	Lys	Thr	Lys	Leu	Val	Gly	Phe	Gln	Asp	
191			95						100					105			
193	atg	gag	tgt	gtg	cct	tgt	gga	gac	cct	cct	cct	cct	tac	gaa	ccg	cac	488
194	Met	Glu	Cys	Val	Pro	Cys	Gly	Asp	Pro	Pro	Pro	Pro	Tyr	Glu	Pro	His	
195			110					115					120				
197	tgt	gcc	agc	aag	gtc	aac	ctc	gtg	aag	atc	gcg	tcc	acg	gcc	tcc	agc	536
198	Cys	Ala	Ser	Lys	Val	Asn	Leu	Val	Lys	Ile	Ala	Ser	Thr	Ala	Ser	Ser	
199		125					130					135					
201	cca	cgg	gac	acg	gcg	ctg	gct	gcc	gtt	atc	tgc	agc	gct	ctg	gcc	acc	584
202	Pro	Arg	Asp	Thr	Ala	Leu	Ala	Ala	Val	Ile	Cys	Ser	Ala	Leu	Ala	Thr	
203	140					145					150				155		
205	gtc	ctg	ctg	gcc	ctg	ctc	atc	ctc	tgt	gtc	atc	tat	tgt	aag	aga	cag	632
206	Val	Leu	Leu	Ala	Leu	Leu	Ile	Leu	Cys	Val	Ile	Tyr	Cys	Lys	Arg	Gln	
207				160						165					170		
209	ttt	atg	gag	aag	aaa	ccc	agc	tgg	tct	ctg	cgg	tca	cag	gac	att	cag	680
210	Phe	Met	Glu	Lys	Lys	Pro	Ser	Trp	Ser	Leu	Arg	Ser	Gln	Asp	Ile	Gln	
211				175					180					185			
213	tac	aac	ggc	tct	gag	ctg	tcg	tgt	ctt	gac	aga	cct	cag	ctc	cac	gaa	728
214	Tyr	Asn	Gly	Ser	Glu	Leu	Ser	Cys	Leu	Asp	Arg	Pro	Gln	Leu	His	Glu	
215			190					195					200				
217	tat	gcc	cac	aga	gcc	tgc	tgc	cag	tgc	cgc	cgt	gac	tca	gtg	cag	acc	776
218	Tyr	Ala	His	Arg	Ala	Cys	Cys	Gln	Cys	Arg	Arg	Asp	Ser	Val	Gln	Thr	
219		205					210					215					
221	tgc	ggg	ccg	gtg	cgc	ttg	ctc	cca	tcc	atg	tgc	tgt	gag	gag	gcc	tgc	824
222	Cys	Gly	Pro	Val	Arg	Leu	Leu	Pro	Ser	Met	Cys	Cys	Glu	Glu	Ala	Cys	
223	220					225					230				235		
225	agc	ccc	aac	ccg	gcg	act	ctt	ggt	tgt	ggg	gtg	cat	tct	gca	gcc	agt	872

RAW SEQUENCE LISTING

DATE: 04/11/2002

PATENT APPLICATION: US/09/380,276A

TIME: 10:26:39

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\04112002\I380276A.raw

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226 Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His Ser Ala Ala Ser
227          240          245          250
229 ctt cag gca aga aac gca ggc cca gcc ggg gag atg gtg ccg act ttc      920
230 Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met Val Pro Thr Phe
231          255          260          265
233 ttc gga tcc ctc acg cag tcc atc tgt ggc gag ttt tca gat gcc tgg      968
234 Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe Ser Asp Ala Trp
235          270          275          280
237 cct ctg atg cag aat ccc atg ggt ggt gac aac atc tct ttt tgt gac      1016
238 Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile Ser Phe Cys Asp
239          285          290          295
241 tct tat cct gaa ctc act gga gaa gac att cat tct ctc aat cca gaa      1064
242 Ser Tyr Pro Glu Leu Thr Gly Glu Asp Ile His Ser Leu Asn Pro Glu
243 300          305          310          315
245 ctt gaa agc tca acg tct ttg gat tca aat agc agt caa gat ttg gtt      1112
246 Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser Gln Asp Leu Val
247          320          325          330
249 ggt ggg gct gtt cca gtc cag tct cat tct gaa aac ttt aca gca gct      1160
250 Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn Phe Thr Ala Ala
251          335          340          345
253 act gat tta tct aga tat aac aac aca ctg gta gaa tca gca tca act      1208
254 Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu Ser Ala Ser Thr
255          350          355          360
257 cag gat gca cta act atg aga agc cag cta gat cag gag agt ggc gct      1256
258 Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln Glu Ser Gly Ala
259          365          370          375
261 atc atc cac cca gcc act cag acg tcc ctc cag gaa gct taaagaacct      1305
262 Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Glu Ala
263 380          385          390
265 gcttcttttct gcagtagaag cgtgtgctgg aacccaaaga gtactccttt gttaggctta      1365
267 tggactgagc agtctggacc ttgcatggct tctggggcaa aaataaatct gaaccaaact      1425
269 gacggcattt gaagcctttc agccagttgc ttctgagcca gaccagctgt aagctgaaac      1485
271 ctcaatgaat aacaagaaaa gactccaggc cgactcatga tactctgcat ctttcctaca      1545
273 tgagaagctt ctctgccaca aaagtgactt caaagacgga tgggttgagc tggcagccta      1605
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281 <211> LENGTH: 417
282 <212> TYPE: PRT
283 <213> ORGANISM: Homo sapiens
285 <220> FEATURE:
286 <221> NAME/KEY: misc_feature
287 <223> OTHER INFORMATION: Origin: human bone marrow stromal cell line HAS303
289 <400> SEQUENCE: 4
291 Met Ala Leu Lys Val Leu Leu Glu Gln Glu Lys Thr Phe Phe Thr Leu
292 -25          -20          -15          -10
295 Leu Val Leu Leu Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Thr Gly
296          -5          -1 1          5
299 Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro

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300          10          15          20
303 Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
304          25          30          35
307 Gly Tyr Gly Glu Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe
308 40          45          50          55
311 Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala
312          60          65          70
315 Val Val Asn Arg Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala
316          75          80          85
319 Ile Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
320          90          95          100
323 Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
324          105          110          115
327 Tyr Glu Pro His Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser
328 120          125          130          135
331 Thr Ala Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser
332          140          145          150
335 Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr
336          155          160          165
339 Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser
340          170          175          180
343 Gln Asp Ile Gln Tyr Asn Gly Ser Glu Leu Ser Cys Leu Asp Arg Pro
344          185          190          195
347 Gln Leu His Glu Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp
348 200          205          210          215
351 Ser Val Gln Thr Cys Gly Pro Val Arg Leu Leu Pro Ser Met Cys Cys
352          220          225          230
355 Glu Glu Ala Cys Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His
356          235          240          245
359 Ser Ala Ala Ser Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met
360          250          255          260
363 Val Pro Thr Phe Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe
364          265          270          275
367 Ser Asp Ala Trp Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile
368 280          285          290          295
371 Ser Phe Cys Asp Ser Tyr Pro Glu Leu Thr Gly Glu Asp Ile His Ser
372          300          305          310
375 Leu Asn Pro Glu Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser
376          315          320          325
379 Gln Asp Leu Val Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn
380          330          335          340
383 Phe Thr Ala Ala Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu
384          345          350          355
387 Ser Ala Ser Thr Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln
388 360          365          370          375
391 Glu Ser Gly Ala Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Glu
392          380          385          390
395 Ala
399 <210> SEQ ID NO: 5

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VARIABLE LOCATION SUMMARY
PATENT APPLICATION: US/09/380,276

DATE: 04/10/2002
TIME: 18:26:56

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\04102002\I380276.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:9; N Pos. 27,28,29,30,31,32,33,34,35